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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OM protein - protein search, using sw model
Published Applications AA:*

1: /cgn2 6/ptodata/1/pubpaa/USO7 PUBCOMB.pep:*

2: /cgn2 6/ptodata/1/pubpaa/USO8 NEW PUB.pep:*

3: /cgn2 6/ptodata/1/pubpaa/USO8 NEW PUB.pep:*

4: /cgn2 6/ptodata/1/pubpaa/USO8 NEW PUB.pep:*

5: /cgn2 6/ptodata/1/pubpaa/USO8 PUBCOMB.pep:*

6: /cgn2 6/ptodata/1/pubpaa/USO8 PUBCOMB.pep:*

7: /cgn2 6/ptodata/1/pubpaa/USO8 PUBCOMB.pep:*

8: /cgn2 6/ptodata/1/pubpaa/USO8 PUBCOMB.pep:*

9: /cgn2 6/ptodata/1/pubpaa/USO8 PUBCOMB.pep:*

10: /cgn2 6/ptodata/1/pubpaa/USO9 PUBCOMB.pep:*

11: /cgn2 6/ptodata/1/pubpaa/USO9 NEW PUB.pep:*

13: /cgn2 6/ptodata/1/pubpaa/USO9 PUBCOMB.pep:*

14: /cgn2 6/ptodata/1/pubpaa/USO0 PUBCOMB.pep:*

15: /cgn2 6/ptodata/1/pubpaa/USO0 PUBCOMB.pep:*

16: /cgn2 6/ptodata/1/pubpaa/USO0 PUBCOMB.pep:*

17: /cgn2 6/ptodata/1/pubpaa/USO0 NEW PUB.pep:*

16: /cgn2 6/ptodata/1/pubpaa/USO0 NEW PUB.pep:*

17: /cgn2 6/ptodata/1/pubpaa/USO0 NEW PUB.pep:*

18: /cgn2 6/ptodata/1/pubpaa/USO0 NEW PUB.pep:*

19: /cgn2 6/ptodata/1/pubpaa/USO0 NEW PUB.pep:*

19: /cgn2 6/ptodata/1/pubpaa/USO0 NEW PUB.pep:*

19: /cgn2 6/ptodata/1/pubpaa/USO0 NEW PUB.pep:*
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Gapop 10.0 , Gapext 0.5
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                  1 MSSAVASAASFLALASASPG.....SWEHAAKLYEDVLLKAKYQW 799
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4276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARI

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15	15	12	<u>ր</u>	15	15	15	25	15	15	15	12	12	14	12	12	14	14	14	12	14	1-1 1-2	14	14	14	14	14	12	14	12
-10-369-453-1918	-10-369-493-190	-10-424-599-2025	-10-369-493-989	-10-369-453-1667	-10-369-453-232	-10-369-453-1835	-10-369-493-751	69-493	-10-369-493-209	-10-369-493-297	-10-425-114-6956	-10-425-114-395	-10-044-543-1	-10-424-599-2161	-10-425-114-528	-10-272-291-	-10-138-075-	-10-044-543-	-10-425-114-5	-10-228-063-	-10-272-291-	-10-272-291-	-10-044-543-	-10-138-075-	-10-044-543-	-10-138-075-	-10-424-59	0-284-663-	-10-425-1
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9180	90	02582	895,	6676,	266,	8358,	516,	4757, Ap	0916,	979,	9569,	9536,	8, Ap	16147	2803,	, Appl	, Appl	2, Ap	,909	, App	, Appl	, Appl	, Appl	, Appl	4, App	, Appl	207776,	•	

## ALIGNMENTS

US-09-952-677-6
US-09-952-677-6
US-09-952-677-6
INCOMPATION:

REQUENCE 6, Application US/09952677

RECORD 1 NOTATION:

REPLICANT: Block, Martina
LOTZ, HOTSE
LULTICKE, Stephanie
Waltez, Lennart
Frohberg, Claus
FROM WHEAT WHICH ARE INVOLVED IN STARCH
ROSSANAN, Jens
SYNTHESIS

NUMBER OF SEQUENCES: 9
CORRESSEE: 1251 Avenue of the Americas
CITY: New York
COUNTRY: United States of Americas
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC COMPATIBLE OF APPLICATION NUMBER: US/09/952,677

RAPPLICATION NUMBER: US/09/952,677
FILING DATE: 19-NO. US20020138976A1-1998
APPLICATION NUMBER: DE 196,390
FILING DATE: 11-SEP-1996
APPLICATION NUMBER: DE 196 3917.7

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LENGTH: 799 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-952-677-6
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Best Local Simi
Matches 764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Haley, Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: AGREVO-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEPHONE: (212) 596-9090
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 28-MAY-1997
ATTORNEY/AGENT INFORMATION:
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                                         721 GVRDTVPPFDPFNHSGLGWTFDRAEAHKLIEALGHCLRTYRDYKESWRGLQERGMSQDFS 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361 GVRKYYKAAGQDMEVNYFHAYIDGVDFVFIDAPLFRHRQEDIYGGSRQEIMKRMILFCKA
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                                                                                                                      HFEREHHDKVRGWVGFSVRLAHRITAGADALLMPSRFEPCGLNQLYAMAYGTVPVVHAVG
                                                                                                                                                                                                                                                                                                                                                                                                QGRGPVDEFPFTELPEHYLEHFRLYDPVGGEHANYFAAGLKWADQVVVVSPGYLWELKTV
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GLRDTVPPFDPFNHSGLGWTFDRAEAHKLIEALGHCLRTYRDFKESWRALQERGMSQDFS
                                                                                      HFEREHHDKVRGWVGFSVRLAHRITAGADALLMPSRFEPCGLNQLYAMAYGTVPVVHAVG
                                                                                                                                                                              LORELGLOVRADVPLLGFIGRLDGOKGVEITADAMPWIVSODVQLVMLGTGRHDLESMLQ
                                                                                                                                                                                                            LQRELGLQVRADVPLLGFIGRLDGQXGVEIIADAMPWIVSQDVQLVMLGTGRHDLESMLR 660
                                                                                                                                                                                                                                                                       EGGWGLHDI IRQNDWKTRGI VNGI DNMEWNPEVDAHLKSDGYTNFSLRTLDSGKROCKEA
                                                                                                                                                                                                                                                                                                     EGGWGLHDIIRQNDWKTRGIVNGIDNWEWNPEVDVHLKSDGYTNFSLGTLDSGKRQCKEA
                                                                                                                                                                                                                                                                                                                                                             QGRGPVDEFPFTELPEHYLEHFRLYDPVGGEHANYFAAGLKWADQVVVVVSPGYLWELKTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVEVPWHVPCGGVPYGDGNLVFIANDWHTALLPVYLKAYYRDHGLMQYTRSIMVIHNIAH
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Pred. No. 3.2e-312;
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Publication No. US20030150023A1
GENERAL INFORMATION:
APPLICANT: EXSeed Genetics
FILLE OF INVENTION: Starch
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/272,291
CURRENT FILING DATE: 2002-10-17
PRIOR APPLICATION NUMBER: 60/329,525
PRIOR APPLICATION NUMBER: 60/329,525
PRIOR FILING DATE: 2001-10-01
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
LENGTH: 641
TYPE: PRT
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929
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 PTSIAEVVAPDSAATISISDKAPESVVPAEKPPPSSGSNFVVSASAPRLDIDSDVEPELK 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 QDAARPPSMNGTPVNGENKSTGGGGATKDSGLPAPARAPHPSTQNRVPVNGENKANVASP 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              493;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAEAEAGGKDAPPERSGDAARLPRARRNA----VSKRRDPLQ----------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QNHDSGPLAGENVMNVVVVAAECSPWCKTGCLGDVAGALPKALAKRGHRVMVVVPRYGDY 354
LESMIRHFEREHHDKVRGWVGFSVRLAHRITAGADALLMPSRFEPCGLNQLYAMAYGTVP
                                                                                                                                WELKTVECGWGLHDIIRSNDWKINGIVNGIDHQEWNPKVDVHLRSDGYTNYSLETLDAGK
                                                                                                                                                                       WELKTVEGGWGLHDIIRQNDWKTRGIVNGIINNMEWNPEVDVHLKSDGYTNFSLGTLDSGK 594
                                            ROCKAALORELGLEVRDDVFLLGFIGRLDG\QKGVDIIGDAMPWIAGQDVQLVMLGTGRAD
                                                                                                                                                                                                                                                                       THNIAHQGRGPVDEFPFTELPEHYLEHFRLYDPVGGEHANYFAAGLKMADQVVVVSPGYL
                                                                                                                                                                                                                                                                                                                      ÍĹ-----GVCYGDGNĹVFÍANDWHTALLÞVYLKAYYRDHGLMQYTRSVLV
                                                                                                                                                                                                                                                                                                                                                                ILFCKAAVEVPWHVPCGGVPYGDGNLVFIANDWHTALLPVYLKAYYRDHGLMQYTRSIMV
                                                                                                                                                                                                                                                                                                                                                                                                               VEAFDMGIRKYYKAAGODLEVNYFHAFIDGVDFVFIDAFLFRHRODDIYGGSROEIMKRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------GIAPPTVEPLVÓEATWDFKKYIGFDEPDEAKDDSRVGÁDDAGSFEHY 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTSIVKFPAPGYRMILPSGDIAPETVLPAPKPLHES-----PAVDGDSN----- 119
                                                                                   ROCKEALORELGLOVRADVELLGFIGRLDGOXGVEIJADAMEWIVSODVOLVMLGTGRHD
                                                                                                                                                                                                                           IHNIAHQGRGPVDEFPYMDLPEHYLQHFELYDPVGGEHANIFAAGLKMADRVVTVSRGYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 2516.5; DB 14; Length 641; Pred. No. 1.7e-189;
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US-10-389-566-797
Sequence 797, Application US/10389566; Publication No. US20040025202A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Laurie, Cathy C
TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
FILE REFERENCE: 38-77(52900)D
CURRENT APPLICATION NUMBER: US/10/389,566
CURRENT FILING DATE: 2003-03-31
PRIOR APPLICATION NUMBER: US 60/365,301
PRIOR APPLICATION NUMBER: US 60/365,301
PRIOR APPLICATION NUMBER: US 60/391,786
PRIOR FILING DATE: 2002-06-25
PRIOR PRIOR DATE: 2002-06-25
PRIOR PRIOR FILING DATE: 2002-06-25
PRIOR FILING DATE: 2002-06-26
NUMBER OF SEQ ID NOS: 2459
SOFTWARE: Patentin version 3.2
SEQ ID NO 797

INVENT: 100
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Best Local (
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473 MVIHNIAHQGRGPVDEFPFTELPEHYLEHFRLYDPVGGEHANYFAAGLKMADQVVVVSPG 532
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                                                                                                 RMILFCKAAVEVPWHVPCGGVPYGDGNLVFIANDWHTALLFVYLKAYYRDHGLMQYTRSI 472
                                                                                                                                                                                     EYAEAKDLGVRKRYRVAGQDSEVSYFHAFIDGVDFVFLEAPPFRHRHNDIYGGERFDVLK 307
                                                                                                                                                                                                                                   DYBEAYDVGVRKYYKAAGQDMEVNYFHAYIDGVDFVFIDAPLFRHRQEDIYGGSRQEIMK 412
                                                                                                                                                                                                                                                                                                             DSENKESGPLAGPNVMNVIVVASECSPFCKTGGLGDVVGALPKALARRGHRVMVVIPRYG 247
                                                                                                                                                                                                                                                                                                                                                                          HHQNHDSGPLAGENVMVVVVVAABCSPWCKTGGLGDVAGALPKALAKRGHRVMVVVPRYG 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELKKGAVIVEEAPNPKALSPPAAPAVQEDLWDFKKYIGFEEPVEAKDDGWAVADDAGSFE 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VSSPKYVKPAVAKONGEVVS---RATKSDAPVSKPK-----VDPSVPASKAEAD--- 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APRODAARPPSMNGTPVNGENKSTGGGGATKDSGLPAPARAPHPSTONRVPVNGENKANV 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MSGALASSPAATLFLAGSSSSSPR-RRRSRVSGVWWHLYGGTGLRLH---WERRGLVRDG 56
                                                               RMILECKAAVEVEWEAPCGGSIYGDGNLVFIANDWHTALLEVYLKAYYRDNGLMQYTRSV 367
                                                                                                                                                                                                                                                                                                                                                                                                                               ------GNAQAVESKAALDKKED-----VGVAEPLEAKADAGGDAGAVSSAD 187
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CURRENT FILING DATE: 2003-03-31
PRIOR APPLICATION NUMBER: US 60/365,301
PRIOR PILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: US 60/391,786
PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/392,018
PRIOR APPLICATION NUMBER: US 60/392,018
PRIOR APPLICATION NUMBER: US 60/392,018
PRIOR PILING DATE: 2002-06-26
NUMBER OF SEQ ID NOS: 2459
SOFTWARE: Patentin version 3.2
SEQ ID NO 1213
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US-10-389-566-1213
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US-10-389-566-1213
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GENERAL INFORMATION:
APPLICANT: Monsento Technology, LLC
APPLICANT: Laurie, Cathy C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1213, Application US/10389566 Publication No. US20040025202A1
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TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
FILE REFERENCE: 38-77(52900)D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 694
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 55.3%; Score 2365.5; DB 16; Length 694; Local Similarity 59.0%; Pred. No. 1.5e-177; Local Similarity 59.0%; Pred. No. 1.5e-177; Baps 476; Conservative 79; Mismatches 131; Indels 121; Gaps
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                                                                                          233 ELKKGAVIVEEAPNPKALSPPAAPAVQEDL#DFKKYIGFEEPVEAKDDGWAVADDAGSFE 292
                                                                                                                                                          101 VŚSPKYVKPAVAKQNGEVVS---RATKSDAFVSKPK-----VDPSVPASKAEAD--- 146
                                                                                                                                                                                                               173 ASPPTSIAEVVAPDSAATISISDKAPESVVFAEKPPPSSGSNFVVSASAPRLDIDSDVEP 232
                                                                                                                                                                                                                                                                                                                                        113 APRODAARPPSMNGTPVNGENKSTGGGGATKDSGLPAPARAPHPSTONRVPVNGENKANV 172
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                                    -GNAQAVESKAALDKKED-----VGVAEPLEAKADAGGDAGAVSSAD 187
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RESULT 5
US-10-044-543-26
; Sequence 26, Application US/10044543
; Publication No. US20030135883A1
; GENERAL INFORMATION:
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; TYPE: PT
; CRCANISM: TYPha latifolia
US-10-044-543-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Singletary, George
APPLICANT: Zhou, Lan
APPLICANT: Zhou, Lan
TITLE OF INVENTION: No. US20030135883A1el Starch Synthase Polynucleotides
TITLE OF INVENTION: and Their Use in the Production of New Starches
FILE REPERENCE: 114D NUMBER: US/10/044,543
CURRENT APPLICATION NUMBER: US/2002-01-11
CURRENT FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: 09/388,743
PRIOR FILING DATE: 1999-09-02
NUMBER OF SEQ ID NOS: 28
SOFTMARE: PastSEQ for Windows Version 3.0
SEQ ID NO 26
SEQ ID NO 26
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Best Local
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                                                                                                                                             192 SI-SDKAPE-----SVVPAEKPPPSSG------------------SNFVVSA-- 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                668 RGMAQDLSWDHAAELYEDVLVKAKYQW 694
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220 SAPRLDIDSDVEPELKKGAVIVEEAPNPKALSPP--AAPAVQEDLWDFKKYIGFEBPVEA 277
                                                                                                                                                                                                                                                           134 KSTGGGGATKDSG--LPAPARAPHPSTQNRVPVNGENKANVASPPTSIAEVVAPDSAATI 191
                                                                                                                                                                                                      21 RATGKSGSFEBEGEEREGVGRAGVGDDALRATIDKSNE--ILAIHSNLLQQIAKRKNIVS 78
                                                                                                                                                                                                                                                                                                                 h 50.6%; Score 2163; DB 14; Length 801; Similarity 60.7%; Pred. No. 1.7e-161; 26; Conservative 84; Mismatches 151; Indels 41
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                                                                                                                                                                                                                                                                                                                    Indels 41;
                                                                                                                                                                                                                                                                                                                                                                                            Publication No. US20040034888A1

Publication No. US20040034888A1

Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Liu, Jingdong

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313)B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 43176

LENGTH: 535

TYPE: PRT
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US-10-425-114-43176
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                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       376 AYYRDNGLMKYARSVLVIHNIAHQGRGPVDDFKFVGLPDHYLDLFRLYDFVGGEHLNIFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    398 RQEDIYGGSRQEIMKRMILFCKAAVEVPWHVPCGGVPYGDGNLVFIANDWHTALLFVYLK 457
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                                                                                           284 VADDAGSFEHHQNHDSGPLAGENVMNVVVVAAECSPWCKTGGLGDVAGALPKALAKRGHR 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              676 NTYWNYKDSWKGLQTRGMMQDLSWDNAAQQYEDVLVAAKYQW 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                758 RTYRDYKESWRGLQERGMSQDFSWEHAAKLYDDVLLKAKYQW 799
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      344 VMVVVPRYGDYEEAYDVGVRKYYKAAGQDMEVNYFHAYIDGVDFVFIDAPLFRHRQEDIY 403
                                                                                                                                                                            386; Conservative
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                                                                  VANEGDNVÉ-SKGENPPÉLAGANVMVILVAAECAPFVKTGGLGDVAGSLPKALARRGHR 79
                                                                                                                                                                      50.5%; Score 2161.5; DB 12; Length 535; 74.8%; Pred. No. 1.3e-161; ative 64; Mismatches 65; Indels 1;
                                                                                                                                                                                Gaps
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US-10-424-599-202586
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APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE OF INVENTION INMEBER: US/10/424,599
CURRENT APPLICANTION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 202586
SEQ ID NO 202586
LENGTH: 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 202586, Application US/10424599 Publication No. US20040031072A1
                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                     Matches 386;
                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Glycine max FEATURE: FATURE: NAME/KEY: unsure LOCATION: (1)..(771)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Clone ID: PAT_MRT3847_24960C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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                                                                                                344 VMVVVPRYGDYSEAYDVGVRKYYKAAGQDMEVNYFHAYIDGVDFVFIDAPLFRHRQEDIY 403
                                                                                                                                                                                                                 284 VADDAGSFEHHQNHDSGFLAGENVMNVVVVAAECSPWCKTGGLGDVAGALPKALAKRGHR 343
                                                                                                                                                                       257 VANEGDNVE-SKGENPPPLAGANVMVILVAAECAPFVKTGGLGDVAGSLPKALARRGHR 315
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                                                                                                                                                                                                                                                                                             l Similarity
GGSRQEIMKRMILFCKAAVEVPWHVPCGGVPYGDGNLVFIANDWHTALLFVYLKAYYRDH
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                                                                           VMVVVPRYSHYADAQDIGVWKRYKVDGQDMEVTYFHSYIDGVDFVFIDSPNFRHLQDNIY 375
                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                50.5%; Score 2161.5; DB 12 74.8%; Pred. No. 2.2e-161; tive 64; Mismatches 65;
                                                                                                                                                                                                                                                                                                                 DB 12; Length 771;
                                                                                                                                                                                                                                                                     Indels
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US-10-284-668-8
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  NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27.794
REFERENCE/DOCKET NUMBER: Agrevo-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEPHONE: 212-596-9090
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 767 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/10284668 Publication No. US20030106100A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/836,567

FILING DATE: 24-UL-1997

APPLICATION NUMBER: PCT/EP95/04415

FILING DATE: 09-NOV-1995

APPLICATION NUMBER: DE P 44 41 408.0

FILING DATE: 10-NOV-1994

ATTORNEY/ACENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
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TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES
INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC
PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Kossmann, Jens
Springer, Franziska
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              704 QLYAMAYGTVPVVHAVGGVRDTVPPFDPFNHSGLGWTFDRAEAHKLIEALGHCLRTYRDY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     584 NFSLGTLDSGKROCKEALORELGLOVRADVPLLGFIGRLDGOKGVEIIADAMPWIVSODV
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                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/10/284,668 FILING DATE: 29-Oct-2002 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QLYAMNYGTIPVVHAVGGLRDTVKPFNPFEESGLGWTFDSAETNKLINALGNCLLTFRQY
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TOPOLOGY: linear;

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-284-668-8
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Matches
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763 AKYOW 767
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                                   AKYOW 799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VIYFQAFIDGVDFVFIDSHMFRHIGNNIYGGNRVDILKRMVLFCKAAIEVPMHVPCGGVC 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AECSPWCKTGGLGDVAGALÆKALAKRGHRVMVVVPRYGDYEEAYDVGVRKYYKAAGQDME 374
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                                                                                                                                                                                                                                                                                                                               WKLQGIVNGIDTKEWNPELDVHLQSDGYMNYSLDTLQTGKPQCKAALQKELGLPVRDDVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VNYFHAYIDGVDFVFIDAPLFRHRQEDIYGGSRQEIMKRMILFCKAAVEVPWHVPCGGVP 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SECAPWSKTGGLGDVAGALÞKALARRGHRVMVVAÞRYDNYÞEPQDSGVRKIYKVDGQDVE 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APAVQEDIMDFKKYIGFEEPVEAKDDGWAVADDAGSFEHHQNHDSGPLAGENVMVVVVA
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                                                                                                                                                           GFSVKTSHRITAGADILLMPSRFEPCGLNQLYAMKYGTIPVVHAVGGLRDTVQPFDPFNE
                                                                                                                                                                                     GFSVRLAHRITAGADALLMPSRFEPCGLNQLYAMAYGTVPVVHAVGGVRDTVPPFDPFNH
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                                                                              SGLGWTFSRAEASQLIHALGNCLLTYREYKKSWEGIQTRCMTQDLSWDNAAQNYEEVLIA 762
                                                                                                                  SGLGWTFDRAEAHKLIEALGHCLRTYRDYKESWRGLQERGMSQDFSWEHAAKLYEDVLLK 794
                                                                                                                                                                                                                                                                                                                                                                   WKTRGIVNGIDNMEWNPEVDVHLKSDGYTNFSLGTLDSGKROCKEALORELGLOVRADVP
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RESULT 9 US-10-272-291-7

Sequence 7, Application US/10272291
Publication No. US20030150023A1
GENERAL INFORMATION:
APPLICANT: ExSeed Genetics
TITLE OF INVENTION: Starch

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; ORGANISM: Zea mays
; PEATURE:
OTHER INFORMATION: Starch Synthase IIb-2 (N-terminally truncated; OTHER INFORMATION: SSIIb)
US-10-272-291-7
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CURRENT PAPELICATION NUMBER: US/10/272,291
CURRENT FILING DATE: 2002-10-17
PRIOR APPLICATION NUMBER: 60/329,525
PRIOR FILING DATE: 2001-10-01
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
SEQ ID NO 7
                                                                                                                                       Sequence 6, Application US/10044543

Publication No. US20030135883A1
GENERAL INFORMATION:
APPLICANT: Singletary, George
APPLICANT: Zhou, Lan
TITLE OF INVENTION: No. US20030135883A1e1 Starch Synthase Polynucleot
TITLE OF INVENTION: and Their Use in the Production of New Starches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local
FILE REFERENCE: 1144D
CURRENT APPLICATION NUMBER: US/10/044,543
CURRENT FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: 09/388,743
PRIOR FILING DATE: 1999-09-02
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             368 AAGQDMEVNYFHAYIDGVDFVFIDAPLFRHRÇEDIYGGSRQBIMKRMILFCKAAVEVPWH 427
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                                                                                                                                                                                                                                                                                                                                                                             466 YEDVLVKAKYOW 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 VAGODSEVTYFHSYIDGVDFVFVEAPPFRHRHMNIYGGERLDILKRMILFCKAAVEVPWY
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RESULT 11
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LENGTH: 690
TYPE: PRT
ORGANISM: Curcuma zedoaria
                                                                                         Sequence 6, Application US/10284668 Publication No. US20030106100A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 48.2%; Score 2063; DB 14; Best Local Similarity 56.0%; Pred. No. 1.1e-153; Matches 404; Conservative 80; Mismatches 166;
APPLICANT: Kossmann, Jens
Springer, Franziska
Springer, Franziska
Abel, Gernot
Abel, Gernot
TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES
INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARTMRFLNALYHGQSADLVPINHRGKSSGAVGRSNIND-IQEDSNQDVDIADDSVAQTME 128
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                                                                                                                                                                                                                     QW 690
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
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COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/00/284,668
FILING DATE: 29-Oct-2002
CLASSIFICATION NUMBER: US/08/356,567
APPLICATION NUMBER: US/08/356,567
APPLICATION NUMBER: US/08/356,567
FILING DATE: 24-UL-1997
APPLICATION NUMBER: PCT/EP95/04415
FILING DATE: 09-NOV-1995
APPLICATION NUMBER: DP 44 41 408.0
FILING DATE: 10-NOV-1994
ATTORMEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: AGTEVO-4
TELEPONNE: 212-596-9000
TELEPAX: 212-596-9000
TELEPAX: 212-596-9090
NEORMATION FOR SEGO ID NO. 6:
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CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of th
CITY: New York
STATE: New York
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 PLAGENVMVVVVAAAECSPWCKTGGLGDVAGJALPKALAKRGHRVMVVVPRYGDYEEAYDV 360
                                  HFEREHHDKVRGWVGFSVRLAHRITAGADALLMPSRFEPCGLNQLYAMAYGTVPVVHAVG
                                                                                                                                            LQRELGLQVRADVPLLGFIGRLDGQKGVEIIADAMFWIVSQDVQLVMLGTGRHDLESMLR 660
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QFECQHNDKIRGWVGFSVKTSHRITAGADIILMPSRFEALRLNQLYAMKYGTIPVVHAVG
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                                                                                                             LOKELGLEVRODVELIGEIGRLDEOKGVOLIABASAWMGQDVQLVMLGTGRRDLEOMLR
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RESULT 12
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APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 38522
LENGTH: 440
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 38552, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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  421
                                                                                                                                                                                                   301
                                                                                                                                                                                                                                                                                                                                           600 ALQREIGLQVRADVPLLGFIGRLDGQKGVEIIADAMPWIVSQDVQLVMLGTGRHDLESML 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         420 AAVEVPWHYPCGGVPYGDGNLVFIANDWHTALLPVYLKAYYRDHGLMQYTRSIMVIHNIA 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   360 VGVRKYYKAAGQDMEVNYFHAYIDGVDFVFIDAPLFRHRQEDIYGGSRQEIMKRMILFCK 419
                                                                                                                                                                                                                                                                                                                                                                                                     181 SEGGWGLHDIINQNDWKLQGIVNGIDMSEWNPAVDVHLHSDDYTNYTFETLDTGKRQCKA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                   540 VEGGWGLHDIIRONDWKTRGIVNGIDNMEWNPEVDVHLKSDGYTNFSLGTIDSGKROCKE 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 HOGRGPVDDFVNFDLPEHYIDHFKLYDNIGGDHSNVFAAGLKTADRVVTVSNGYMWELKT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     480 HQGRGPVDEFPFTELPEHYLEHFRLYDPVGGEHANYFAAGLKMADQVVVVVSEGYLWELKT 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 AAVEVPWYAPCGGTVYGDGNLVFIANDWHTALLPVYLKAYYRDNGLMQYARSVLVIHNIA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WEHAAKLYEDVLIKAKYQW 799
|::||:||:||:||||
| HILLIKAKYQW 558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GVRDTVPPFDPFNHSGLGWTFDRAEAHKLIEALGHCLRTYRDYKESWRGLQERGMSQDFS
SWDHAAVLYEDVLVKAKYQW 440
                                                   SWEHAAKLYEDVLLKAKYOW 799
                                                                                                    GGLRDTVAPFDFFNDTGLGWTFDRAEANRMIDALSHCLTTYRNYKESWRGLQARGMAQDL 420
                                                                                                                               GGVRDTVPPFDPFNHSGLGWTFDRAEAHKLIEALGHCLRTYRDYKESWRGLQERGMSQDF 779
                                                                                                                                                                                                   RRFESEHSDKVRAWVGFSVPLAHRITAGADILLMPSRFEPCGLNQLYAMAYGTVPVVHAV 360
                                                                                                                                                                                                                                                  RHFEREHHDKVRGWVGFSVRLAHRITAGADALLMPSRFEPCGLNQLYAMAYGTVPVVHAV 719
                                                                                                                                                                                                                                                                                                   ALQRQLGLQVRDDVPLIGFIGRLDHQKGVDIIADAIHWIAGQDVQLVMLGTGRADLEDML 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGVRRRYKVAGODSEVTYFHSYIDGVDFVFVBAPPFRHRHNNIYGGERLDILKRMILFCK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45.2%; Score 1933; DB 12; Length 44
79.1%; Pred. No. 1e-143;
7ative 40; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 440;
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US-10-425-114-58577

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US-10-284-668-10
S-10-284-668-10
Sequence 10, Application US/10284668
Publication No. US20030106100A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT APPLICATION SEQ ID NOS: 73128
SEQ ID NO 58577
LENGTH: 3311
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Publication No. US20040034888A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 238; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 32.1%; Score 1374; DB 12; Local Similarity 69.8%; Pred. No. 8.4e-100;
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
                                                                                                                                                                                                                                                      TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES
INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC
PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES
                                                                                                                                                                                                                                                                                                                                    APPLICANT: Kossmann, Jens
Springer, Franziska
Abel, Gernot
                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  579 SDGYTNFSLGTLDSGKRQCKEALQRELGLQVRADVPLLGFIGELDGQKGVEIIADAMPWI 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       519 GLKMADQVVVVSPGYLWELKTVEGGWGLHDIIRQNDWKTRGIVNGIDNMEWNPEVDVHLK 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             459 YYRDHGIMQYTRSIMVIHNIAHQGRGPVDEFPFTELPEHYLEHFRLYDPVGGEHANYFAA 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 TYRNYWSSWEGIORRGMMODLSWDNAAKLYEEVILAAKYOW 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 AGODVOLIMIGTGRODLEDTIRRLESOHYDRVRGWVGFSVRLAHRMTAGADILIMPSRFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  639 VSQDVQLVMLGTGRHDLESMLRHFEREHHDKVRGWVGFSVRLAHRITAGADALLMPSRFE 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GIRAADRILITVSHGYAWELKTPDGGWGLHSIINENDWKFQGIVNGIDTADWNPRHDVHLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 YYRDNGFMPYARSVLVIHNIAHQGRGPIDDENYLDLÞGHYMDQFKLYDÞFGGDHLNIFAA
                                                                             CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SDGYTNYSLETVQTGKAQCKEALQKELGLEVXGDVPVIAFIGRLDHQKGVDLIAEANEWI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYRDYKESWRGLQERGMSQDFSWEHAAKLYEDVLLKAKYQW 799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCGLNOLYAMWYGTVPVVHAVGGLRDTVQHYNPYBEVGVGWTFEKAEANRMIDALGHCLN 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCGLNQLYAMAYGTVPVVHAVGGVRDTVPPFDPFNHSGLGWTFDRAEAHKLIEALGHCLR 758
                                                                                                                                                           STREET: 1251 Avenue of the Americas
                                                                                                         York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51; Mismatches 52;
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Query Match 27.5%; Score 1176; DB 14; Length Best Local Similarity 45.2%; Pred. No. 8.3e-84; Matches 250; Conservative 72; Mismatches 181; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        331 GALPKALAKRGHRVMVVVPRY------GDYEEAYDVGVRKYYKAAGQDMEVNYFHAYID 383
                                                                                                                                                                                                                                                                                                                                                                                                                             390 SSRQSVLNGITNGIDYNDWNPSTDEHIAS----HYSINDL-SGKVQCKTDLQKELGLPIR 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154 GSLPMALAARGHRVMVVSPRYLNGGPSDEKYANAVDLDVRATVHCFGDAQEVAFYHEYRA 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          283 AVADDAGSFEHHQ--NHDSGPLAGEN------VMNVVVVAAECSPWCKTGGLGDVA 330
                                                                                                                                                                                                                                                              671 RGWVGFSVRLAHRITAGADALLMPSRFEPCGLNQLYAMAYGTVPVVHAVGGVRDTVPPFD 730
                                                                                                                                                                                                                                                                                                                                                                                 611 ADVPLLGFIGRLDGOKGVEIIADAMPWIVSQDVQLVMLGTGRHDLESMLRHFEREHHDKV 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   551 RONDWKTRGIVNGIDNMEWNPEVDVHLKSDGYTNFSLGTLDSGKRQCKEALQRELGLQVR 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                330 YGAVEWIFPTWARAHALDTGETVNVLKGAIAVADRILTVSQGYSWEITTPEGGYGLHELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   499 LEHFRLYDPV------GGEHANYFAAGLKWADQVVVVSPGYLWELKTVEGGWGLHDII 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               270 KCLFLANDWHAALVFLLLAAKYRPYGVYKDARSIVAIHNIAHQGVEPAVTYNNLGLPPQW 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  439 NLVFIANDWHTALLPVYLKAYYRDHGLMQYTRSIMVIHNIAHQGRGPVDEFPFTELPEHY 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        384 GVDFVFIDAPLFRH---RQEDIYG--GSRQEIMKRMILFCKAAVEVPWHVPCGGVPYGDG 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94 SVÁGDÁTMVÉSÁDIVANDRODÍSEDTEEMEETPIKLTFNIIFVTÁÉAAPYSKTGGÍGDVC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVDWVFVDHSSYCRPGTPYGDIYGAFGDNQ---FRFTLLSHAACEAPLVLPLGGFTYGE- 269
                                                                                         PYAQEGIGEGTGWTFSPLTSEKLLDTLKLAIGTYTEHKSSWEGLMRRGMGRDYSWENAAI 624
                                                                                                                                                                                                        RAWVGFNVPVSHRITAGCDILLMPSRFEPCGLNQLYAMRYGTIPIVHSTGGLRDTVKDFN 564
                                                                                                                                            PFNHSGL----GWTFDRAEAHKLIEALGHCLRTYRDYKESWRGLQERGMSQDFSWEHAAK 786
                                                                                                                                                                                                                                                                                                                           PDCPLIGFIGRLDYQKGVDIILSAIPELMQNDVQVVMLGSGEKQYEDWMRHTENLFKDKF
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SOFTWARE: Patentin Neturn
CURRENT APPLICATION NUMBER: US/09/952,677
APPLICATION NUMBER: US/09/952,677
FILING DATE: 14-Sep-2001
PRICR APPLICATION NUMBER: 09/196,390
FILING DATE: 19-NO. US20020138876A1-1998
APPLICATION NUMBER: DE 196 21 588.9
FILING DATE: 19-NAY-1996
APPLICATION NUMBER: DE 196 36 917.7
FILING DATE: 29-MAY-1996
APPLICATION NUMBER: DE 196 36 917.7
FILING DATE: 11-SEP-1996
APPLICATION NUMBER: DET/EP97/02793
FILING DATE: 28-MAY-1996
APPLICATION NUMBER: 27,794
REFIRENCE/DOCKET NUMBER: 27,794
REFIRENCE/DOCKET NUMBER: 37,794
REFIRENCE/DOCKET NUMBER: 396-9000
FILERANICATION INFORMATION:
FILERANICATION SPG-9000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 671 amino acids
TOPOLOGY: 11near
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-952-677-2

US-09-952-677-2

AT-OR SEG ID NO: 2:
US-09-952-677-2
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US-09-952-677-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEB: James F. Haley, Jr., 2/o
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Frohberg, Claus
Kossmann, Jens
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING ENZYMES
FROM WHEAT WHICH ARE INVOLVED IN STARCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Block, Martina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
115 HIKIPCFGGSHEVTFFHEYRDNVDWVFVDHPSY-HRPGSLYGDNFGAFGDNQFRYTLLCY 173
                                                                                                                                                                  365 YYK--AAGQDMEVNYFHAYIDGVDEVFIDAPLERHEQEDIYG---GSRQEIMKRMILFCK 419
                                                                                                                                                                                                                                                                                           309 NVVVVAAECSPWCKTGGLGDVAGALPKALAKRGHRVMVVVPRY----GDYBBAYDVGVRK 364
                                                                                                                                                                                                                                     55 SIVFYTGEAAÞYAKSGGLGDVCGSLÞIALAARGHRVMVVMÞRÝLNGSSDKNYÁKALYTAK 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: New York
                                                                                                                                                                                                                                                                                                                                                    26.6%; Score 1138.5; DB 9; Length ilarity 47.8%; Pred. No. 8=-81; Conservative 71; Mismatches 161; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lutticke, Stephanie
Walter, Lennart
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                                                                                                                                                                                                                                                                                                                                                                                                             DB 9; Length 671;
                                                                                                                                                                                                                                                                                                                                                           27;
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US-10-284-668-10

214

TELEFAX: 212-596-9090 INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:

LENGTH: 641 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:

APPLICATION NUMBER: PCT/EP95/04415
FILING DATE: 09-NOV-1995
APPLICATION NUMBER: DE P 44 41 408.0
FILING DATE: 10-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haley dr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: Agrevo-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEPHONE: 212-596-9000

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/836,567
FILING DATE: 24-JUL-1997

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/284,668 FILING DATE: 29-Oct-2002

CLASSIFICATION: <Unknown>

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Search completed: March 17, 2004, 19:37:08 Job time: 47 secs
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